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CLAIMS

1. A method for simultaneously detecting deletions at a plurality of DNA sequences, comprising the steps of:

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treating said DNA to form single-stranded complementary strands;

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adding a plurality of paired oligonucleotide primers, each pair specific for a different sequence, one primer of each pair substantially complementary to a part of the sequence in the sense-strand and the other primer of each pair substantially complementary to a different part of the same sequence in the complementary anti-sense strand;

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annealing the plurality of primers to their complementary sequences;

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simultaneously extending said plurality of annealed primers from each primer's 3' terminus to synthesize an extension product complementary to the strands annealed to each primer, said extension products, after separation from their complement, serving as templates for the synthesis of an extension product from the other primer of each pair;

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separating said extension products from said templates to produce single-stranded molecules;

amplifying said single stranded molecules by repeating, at least once, said annealing, extending and separating steps; and

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identifying said amplified extension products from each different sequence.

2. The method of Claim 1 for detecting deletions at a plurality of genomic DNA sequences, wherein said sequences are selected from the group of sequences on the X and Y chromosomes.

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3. The method of Claim 2 for the detection of X-linked disease, wherein said genomic DNA sequences

1 contain a deletion that causes a genetic disease.

4. The method of Claim 3 for the detection of said X-linked genetic diseases selected from the group consisting of ornithine transcarbamylase deficiency, hypoxanthine phosphoribosyltransferase deficiency, steroid sulfatase deficiency and X-linked muscular dystrophy.

5. The method of Claim 4 for the detection of X-linked muscular dystrophy, wherein said plurality of paired primers are complementary to different sequences within the gene coding for the dystrophin protein.

6. The method of Claim 5, wherein the plurality of paired primers is selected from the group consisting of:

(1) 5'-GACTTTCGATGTTGAGATTACTTTCCC-3'

(2) 5'-AAGCTTGAGATGCTCTCACCTTTTCC-3',

(1) 5'-GTCCTTTACACACTTTACCTGTTGAG-3'

(2) 5'-GGCCTCATTCTCATGTTCTAATTAG-3',

(1) 5'-AAACATGGAACATCCTTGTGGGGAC-3'

(2) 5'-CATTCCTATTAGATCTGTCGCCCTAC-3',

(1) 5'-GATAGTGGGCTTTACTTACATCCTTC-3'

(2) 5'-GAAAGCACGCAACATAAGATACACCT-3',

(1) 5'-CTTGATCCATATGCTTTTACCTGCA-3'

(2) 5'-TCCATCACCTTCAGAACCTGATCT-3',

(1) 5'-GAATACATTGGTTAAATCCCAACATG-3'

(2) 5'-CCTGAATAAAGTCTTCCTTACCACAC-3', and

(1) 5'-TTCTACCACATCCCATTTTCTTCCA-3'

(2) 5'-GATGGCAAAAGTGTTGAGAAAAAGTC-3'.

-36-

1 7. The method of Claim 3, wherein said genomic DNA is from fetal tissue.

5 8. The method of Claim 1 for detecting deletions at a plurality of genomic DNA sequences, wherein the plurality of paired primers is selected from the group consisting of:

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- 10 (1) 5'-GACTTTCGATGTTGAGATTACTTTCCC-3'
(2) 5'-AAGCTTGAGATGCTCTCACCTTTTCC-3',
- (1) 5'-GTCCTTTACACACTTTACCTGTTGAG-3'
(2) 5'-GGCCTCATTCTCATGTTCTAATTAG-3',
- (1) 5'-AAACATCGAACATCCTTGTGGGGAC-3'
(2) 5'-CATTCCTATTAGATCTGTGCGCCCTAC-3',
- 15 (1) 5'-GATAGTGGGCTTTACTTACATCCTTC-3'
(2) 5'-GAAAGCACGCAACATAAGATACACCT-3',
- (1) 5'-CTTGATCCATATGCTTTTACCTGCA-3'
(2) 5'-TCCATCACCTTCAGAACCTGATCT-3',
- (1) 5'-GAATACATTGGTTAAATCCCAACATG-3'
(2) 5'-CCTGAATAAAGTCTTCTTACCACAC-3',
- 20 (1) 5'-TTCTACCACATCCCATTCTTCCA-3'
(2) 5'-GATGGCAAAAGTGTTGAGAAAAGTC-3',
- (1) 5'-TGGTCTCCTTAAACCTGTCTT-3'
(2) 5'-ACACAACTGTGTTCACTAG-3',
- (1) 5'-ACGTGGAGTGACGATGCTCTTCCC-3'
(2) 5'-GTGGGATTCACTACTTTTCCC-3', and
- 25 (1) 5'-GAAGTCAAGGACACCGAGGAA-3'
(2) 5'-AGCCCTCTGGCCAGTCCTAGTG-3'.

9. A DNA sequence of the formula:

5'	10	20	30	40	50
TAAATTGACT	TTCGATGTTG	AGATTACTTT	CCCTTGCTAT	TTCAGTGAAC	
60	70	80	90	100	
CAAACCTTAAG	TCAGATAAAA	CAATTTTATT	TGGCTTCAAT	ATGGTGCTAT	
110	120	130	140	150	
TTTGATCTGA	AGGTCAATCT	ACCAACAAGC	AAGAACAGTT	TCTCATTATT	
160	170	180	190	200	
TTCCTTTGCC	ACTCCAAGCA	GTCTTTACTG	AAGTCTTTCG	AGCAATGTCT	
210	220	230	240	250	
GACCTCTGTT	TCAATACTTC	TCACAGATTT	CACAGGCTGT	CACCACCACT	
260	270	280	290	300	
CAGCCATCAC	TAACACAGAC	AAGTGTAAATG	GAAACAGTAA	CTACGGTGAC	

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1	310	320	330	340	350
	CACAAGGGAA	CAGATCCTGG	TAAAGCATGC	TCAAGAGGAA	CTTCCACCAC
	360	370	380	390	400
	CACCTCCCCA	AAAGAAGAGG	CAGATTACTG	TGGATTCTGA	AATTAGGAAA
	410	420	430	440	450
5	AGGTGAGAGC	ATCTCAAGCT	TTTATCTGCA	AATGAAGTGG	AGAAAACCTCA
	460	470	480	490	500
	TTTACAGCAG	TTTTGTTGGT	GGTGTTTTCA	CTTCAGCAAT	ATTTCCAGAA
	510	520	530	540	550
	TCCTCGGGTA	CCTGTAATGT	CAGTTAATGT	AGTGAGAAAA	ATTATGAAGT
	560	570	580	590	600
	ACATTTTAAA	ACTTTCACAA	GAAATCACTA	TCGCAACAGA	AACTAAATGC
	610	620	630	640	650
10	TTAATGGAAA	TGGTGTTC	TGGGGTGAAA	GAAGAACTA	TAGAAACTAT
	660	670	680	690	700
	AGGTGATAAA	CTACTGTGGT	AGCATTTTAA	TCCTAAAAGT	TTCTTTCTTT
	710	720	730	740	750
	CTTTTTTTTT	TTTCTTCCTT	ATAAAGGGCC	TGCTTGTTGA	GTCCCTAGTT
	760	770	780	790	800
	TTGCATTAAA	TGTCTTTT	TTCCAGTAAC	GGAAAGTGCA	TTTTTCATGAA
	810	820	830	840	850
15	GAAGTACACC	TATAATAGAT	GGGATCCATC	CTGGTAGTTT	ACGAGAACAT
	860	870	880	890	900
	GATGTCTCAG	TCTGCGCATC	CTAAATCAGG	AGTAATTACA	GAACACATTT
	910	920	930	940	950
	CCTGTTCTTT	GATATTTATA	AAGTCTTATC	TTGAAGGTGT	TAGAATTTTT
	960	970	980	990	1000
	AACTGATCTT	TTTGTGACTA	TTCAGAATTA	TGCATTTTAT	ATAAGATTAG
20	1010	1020	1030	1040	
	GTATTATGTA	AATCAGTGGA	TATATTAAAT	GATGGCAATA	A-3'

and fragments and derivatives thereof, said fragments and derivatives complementary to the sense and anti-sense strands of the gene coding for dystrophin, said fragments and derivatives capable of annealing to said strands of the dystrophin gene and amplifying dystrophin sequences.

10. A DNA sequence of the formula:

5'	10	20	30	40	50
TGTCCAAAAT	AGTTGACTTT	CTTTCTTTAA	TCAATAAATA	TATTACTTTA	
60	70	80	90	100	
AAGGGAAAAA	TTGCAACCTT	CCATTTAATA	TCAGCTTTAT	ATTGAGTATT	
110	120	130	140	150	
TTTTTAAAAT	GTTGTGTGTA	CATGCTAGGT	GTGTATATTA	ATTTTATTTT	
160	170	180	190	200	
GTTACTTGAA	ACTAAACTCT	GCAAATGCAG	GAAACTATCA	GAGTGATATC	
210	220	230	240	250	
TTTGTCTAGTA	TAACCAAAAA	ATATACGCTA	TATCTCTATA	ATCTGTTTAA	
260	270	280	290	300	
CATAATCCAT	CTATTTTCT	TGATCCATAT	GCTTTTACCT	GCAGGCGATT	

1 310 320 330 340 350
 TGACAGATCT GTTGAGAAAT GGCGGCGTTT TCATTATGAT ATAAAGATAT
 360 370 380 390 400
 TTAATCAGTG GCTAACAGAA GCTGAACAGT TTCTCAGAAA GACACAAATT
 410 420 430 440 450
 5 CCTGAGAAAT GGGAACATGC TAAATACAAA TGGTATCTTA AGGTAAGTCT
 460 470 480 490 500
 TTGATTTGTT TTTTCGAAAT TGTATTTATC TTCAGCACAT CTGGACTCTT
 510 520 530 540 550
 TAACTTCTTA AAGATCAGGT TCTGAAGGGT GATGGAAATT ACTTTTGACT
 560 570 580
 GTTGTGTGCA TCATTATATT ACTAGAAAGA AAA-3'

10 and fragments and derivatives thereof, said fragments and
 derivatives complementary to the sense and anti-sense
 strands of the gene coding for dystrophin, said fragments
 and derivatives capable of annealing to said strands of
 the dystrophin gene and amplifying dystrophin sequences.

15 11. A DNA sequence of the formula:

5' 10 20 30 40 50
 ACCCAAATAC TTTGTTCATG TTTAAATTTT ACAACATTTT ATAGACTATT
 60 70 80 90 100
 AAACATGGAA CATCCTTGTG GGGACAAGAA ATCGAATTGG CTCTTGAAAA
 110 120 130 140 150
 GGTTCCTAAC TAATTGATTT GTAGGACATT ATAACATCCT CTAGCTGACA
 20 160 170 180 190 200
 AGCTTACAAA AATAAAACT GGAGCTAACC GAGAGGGTGC TTTTTCCTCT
 210 220 230 240 250
 GACACATAAA AGGTGCTCTT CTGTCTTGTA TCCTTTGGAT ATGGGCATGT
 260 270 280 290 300
 CAGTTTCATA GGGAAATTTT CACATGGAGC TTTTGTATTT CTTTCTTTGC
 310 320 330 340 350
 25 CAGTACAAC TGCATGTGGTA GCACACTGTT TAATCTTTTC TCAAATAAAA
 360 370 380 390 400
 AGACATGGGG CTCATTTTTT GTTTTGCCTT TTTGGTATCT TACAGGAAC T
 410 420 430 440 450
 CCAGGATGGC ATTGGGCAGC GGCAAACTGT TGTCAGAACA TTGAATGCAA
 460 470 480 490 500
 CTGGGGAAGA AATAATTGAG CAATCCTCAA AAACAGATGC CAGTATTCTA
 510 520 530 540 550
 30 CAGGAAAAAT TGGGAAGCCT GAATCTGCGG TGGCAGGAGG TCTGCAAACA
 560 570 580 590 600
 GCTGTCAGAC AGAAAAAGA GGTAGGGCGA CAGATCTAAT AGGAATGAAA
 610 620
 ACATTTTAGC AGACTTTTAA AGCTT-3'

and fragments and derivatives thereof, said fragments and
 35 derivatives complementary to the sense and anti-sense

strands of the gene coding for dystrophin, said fragments and derivatives capable of annealing to said strands of the dystrophin gene and amplifying dystrophin sequences.

12. A DNA sequence of the formula:

5' 10 20 30 40 50
TTTTGTAGAC GGTTAATGAA TAATTTTGAA TACATTGGTT AAATCCCAAC
60 70 80 90 100
ATGTAATATA TGTAATAAAT CAATATTATG CTGCTAAAAT AACACAAATC
110 120 130 140 150
AGTAAGATTC TGTAATATTT CATGATAAAT AACTTTTGAA AATATATTTT
160 170 180 190 200
TAAACATTTT GCTTATGCCT TGAGAATTAT TTACCTTTTT AAAATGTATT
210 220 230 240 250
TTCCTTTCAG GTTTCAGAG CTTTACCTGA GAAACAAGGA GAAATTGAAG
260 270 280 290 300
CTCAAATAAA AGACCTTGGG CAGCTTGAAA AAAAGCTTGA AGACCTTGAA
310 320 330 340 350
GAGCAGTTAA ATCATCTGCT GCTGTGGTTA TCTCCTATTA GGAATCAGTT
360 370 380 390 400
GGAAATTTAT AACCAACCAA ACCAAGAAGG ACCATTGAC GTTAAGGTAG
410 420 430 440 450
GGGAACTTTT TGCTTTAATA TTTTGTCTT TTTTAAGAAA AATGGCAATA
460 470 480 490 500
TCACTGAATT TTCTCATTTG GTATCATTAT TAAAGACAAA ATATTACTTG
510 520 530 540 550
TTAAAGTGTG GTAAGGAAGA CTTTATTCAG GATAACCACA ATAGGCACAG
560 570 580 590 600
GGACCACTGC AATGGAGTAT TACAGGAGGT TGGATAGAGA GAGATTGGGC
610 620 630 640 650
TCAACTCTAA ATACAGCACA GTGGAAGTAG GAATTTATAG C-3'

and fragments and derivatives thereof, said fragments and derivatives complementary to the sense and anti-sense strands of the gene coding for dystrophin, said fragments and derivatives capable of annealing to said strands of the dystrophin gene and amplifying dystrophin sequences.

13. A DNA sequence of the formula:

5' 10 20 30 40 50
TGAGAAATAA TAGTTCCGGG GTGACTGATA GTGGGCTTTA CTTACATCCT
60 70 80 90 100
TCTCAATGTC CAATAGATGC CCCCAAATGC GAACATTCCA TATATTATAA
110 120 130 140 150
ATTCTATTGT TTTACATTGT GATGTTTCAAT AATAAGTTGC TTTCAAAGAG
160 170 180 190 200
GTCATAATAG GCTTCTTTCA AATTTTCAGT TTACATAGAG TTTTAATGGA
210 220 230 240 250
TCTCCAGAAT CAGAAACTGA AAGAGTTGAA TGACTGGCTA ACAAACAGA

1	260	270	280	290	300
	AGAAAGAACA	AGGAAAATGG	AGGAAGAGCC	TCTTGGACCT	GATCTTGAAG
	310	320	330	340	350
	ACCTAAAACG	CCAAGTACAA	CAACATAAGG	TAGGTGTATC	TTATGTTGCG
	360	370	380	390	400
5	TGCTTTCTAC	TAGAAAGCAA	ACTCTGTGTA	TAGTACCTAT	ACACAGTAAC
	410	420	430	440	450
	ACAGATGACA	TGGTTGATGG	GAGAGAATTA	AAACTTAAAG	TCAGCCATAT
	460	470	480	490	500
	TTTAAAAATT	ATTTTACCT	AATTGTTTTT	GCAATCTTTG	TTGCCAATGG
	510	520	530	540	550
	CCTTGAATAA	GTCCCCTCCA	AAATTCAGGT	GATTGTATTA	GGAGATGGAA
	560	570	580	590	600
10	TATTTAAGGG	TGAATAATCC	ATCAGGGCTC	CTCCCTTAAG	AATAGGATCA
	610	620	630	640	650
	AGTCCCATAT	AAAAGAGGCT	TCACACAGTG	TTCTCCTATC	TCTTGACCCT
	660	670	680	690	700
	CCACCATGCA	CCACCATGTG	AAAACCTCTGT	GAAAAGGCCC	TCACCAGATG
	710	720	730	740	750
	CTAACATCTT	GATCTTGGAT	TTCCCAAAC	CGAGAACTGT	GAAAAAATAA
	760	770	780	790	800
15	AGGTACATTC	TTCCTAAATT	ACCTCATTCT	CATTTAAACA	CACAAAGTGC
	810				
	ACACATAGCT	G-3'			

and fragments and derivatives thereof, said fragments and derivatives complementary to the sense and anti-sense strands of the gene coding for dystrophin, said fragments and derivatives capable of annealing to said strands of the dystrophin gene and amplifying dystrophin sequences.

14. A DNA sequence of the formula:

5'	10	20	30	40	50
25	TTACTGGTGG	AAGAGTTGCC	CCTGCGCCAG	GGAATTCTCA	AACAATTAAA
	60	70	80	90	100
	TGAAACTGGA	GGACCCGTGC	TTGTAAGTGC	TCCCATAGC	CCAGAAGAGC
	110	120	130	140	150
	AAGATAAACT	TGAAAATAAG	CTCAAGCAGA	CAAATCTCCA	GTGGATAAAG
	160	170	180	190	200
	GTTAGACATT	AACCATCTCT	TCCGTCACAT	GTGTAAATG	TTGCAAGTAT
	210	220	230	240	250
30	TTGTATGTAT	TTTGTTCCT	GGGTGCTTCA	TTGGTCGGG	AGGAGGCTGG
	260	270	280		
	TATGTGGATT	GTTGTTTGT	TTTGTTTTTT-3'		

and fragments and derivatives thereof, said fragments and derivatives complementary to the sense and anti-sense strands of the gene coding for dystrophin, said fragments and derivatives capable of annealing to said strands of

the dystrophin gene and amplifying dystrophin sequences.

15. A DNA sequence of the formula:

5' 10 20 30 40 50
AAGCTTTGAT ACTGTGCTTT AAGTGTTTAC CCTTTGGAAA GAAAATAATT
5 60 70 80 90 100
TTGACAGTGA TG TAGAAATA ATTATTTGAT ATTTATTTCA AAACAAAATT
110 120 130 140 150
TATATCCAAT ACTAAACACA GAATTTTGTA AAACAATAAG TGTATAAAGT
160 170 180 190 200
AAAATGAACA TTAGGATTAT TGAGATTATT GTAGCTAAAA CTAGTGTTTA
210 220 230 240 250
10 TTCATATAAA TTATGTTAAT AAATTGTATT GTCATTATTG CATTTTACTT
260 270 280 290 300
TTTTGAAAAG TAGTTAATGC CTGTGTTTCT ATATGAGTAT TATATAATTC
310 320 330 340 350
AAGAAGATAT TGGATGAATT TTTTTTTTAA GTTTAATGTG TTTCACATCT
360 370 380 390 400
CTGTTTCTTT TCTCTGCACC AAAAGTCACA TTTTGTGCC CTTATGTACC
410 420 430 440 450
15 AGGCAGAAAT TGATCTGCAA TACATGTGGA GTCTCCAAGG GTATATTTAA
460 470 480 490 500
T520x ATTTAGTAAT TTTATTGCTA ACTGTGAAGT TAATCTGCAC TATATGGGTT
510 520 530 540 550
CTTTTCCCA GGAAACTGAA ATAGCAGTTC AAGCTAAACA ACCGGATGTG
560 570 580 590 600
GAAGAGATTT TGTCTAAAGG GCAGCATTTG TACAAGGAAA AACCAGCCAC
610 620 630 640 650
20 TCAGCCAGTG AAGGTAATGA AGCAACCTCT AGCAATATCC ATTACCTCAT
660 670 680 690 700
AATGGGTAT GCTTCGCCTG TTGTACATTT GCCATTGACG TGGACTATTT
710 720 730 740 750
ATAATCAGTG AAATAACTTG TAAGGAAATA CTGGCCATAC TGTAATAGCA
760 770 780 790 800
GAGGCAAAGC TGTCTTTTGT ATCAGCATAT CCTATTTATA TATTGTGATC
810 820 830 840
25 TTAAGGCTAT TAACGAGTCA TTGCTTTAAA GGACTCATT TCGTC-3'

and fragments and derivatives thereof, said fragments and derivatives complementary to the sense and anti-sense strands of the gene coding for dystrophin, said fragments and derivatives capable of annealing to said strands of the dystrophin gene and amplifying dystrophin sequences.

16. A DNA sequence of the formula:

5' 103 113 123 133 143
CCCATCTTGT TTTGCCTTTG TTTTCTTG AATAAAAAA AAATAAGTAA
153 163 173 183 193
35 AATTTATTTT CCTGGCAAGG TCTGAAACT TTTGTTTCT TTACCACTTC

1	203	213	223	233	243
	CACAATGTAT	ATGATTGTTA	CTGAGAAGGC	TTATTTAACT	TAAGTTACTT
	253	263	273	283	293
	GTCCAGGCAT	GAGAATGAGC	AAAATCGTTT	TTTAAAAAAT	TGTAAATGT
	303	313	323	333	343
5	ATATTAATGA	AAAGGTTGAA	TCTTTTCATT	TTCTACCATG	TATTGCTAAA
	353	363	373	383	393
	CAAAGTATCC	ACATTGTTAG	AAAAAGATAT	ATAATGTCAT	GAATAAGAGT
	403	413	423	433	443
	TTGGCTCAAA	TTGTTACTCT	TCAATTAAAT	TTGACTTATT	GTTATTGAAA
	453	463	473	483	493
	TTGGCTCTTT	AGCTTGTGTT	TCTAATTTTT	CTTTTTCTTC	TTTTTTCCTT
	503	513	523	533	543
10	TTTGCAAAAA	CCCAAAATAT	TTTAGCTCCT	ACTCAGACTG	TTACTCTGGT
	553	563	573	583	593
	GACACAACCT	GTGGTTACTA	AGGAAACTGC	CATCTCCAAA	CTAGAAATGC
	603	613	623	633	643
	CATCTTCCTT	GATGTTGGAG	GTACCTGCTC	TGGCAGATTT	CAACCGGGCT
	653	663	673	683	693
	TGGACAGAAC	TTACCGACTG	GCTTTCTCTG	CTTGATCAAG	TTATAAAATC
	703	713	723	733	743
15	ACAGAGGGTG	ATGGTGGGTG	ACCTTGAGGA	TATCAACGAG	ATGATCATCA
	753	763	773	783	793
	AGCAGAAGGT	ATGAGAAAAA	ATGATAAAAG	TTGGCAGAAG	TTTTTCTTTA
	803	813	823	833	843
	AAATGAAGAT	TTTCCACCAA	TCACTTTACT	CTCCTAGACC	ATTTCCCACC
	853	863	873	883	893
	AGTTCTTAGG	CAACTGTTTC	TCTCTCAGCA	AACACATTAC	TCTCACTATT
20	903	913	923	933	943
	CAGCCTAAGT	ATAATCAGGT	ATAAATTAAT	GCAAATAACA	AAAGTAGCCA
	953	963	973	983	993
	TACATTAAAA	AGGAAAATAT	ACAAAAAATA	AAAAAATAAA	AAGCCAGAAA
	1003	1013			
	CCTACAGAAT	AGTGCTCTAG	TAATTAC 3'		

25 and fragments and derivatives thereof, said fragments and derivatives complementary to the sense and anti-sense strands of the gene coding for dystrophin, said fragments and derivatives capable of annealing to said strands of the dystrophin gene and amplifying dystrophin sequences.

30 17. A DNA sequence of the formula:

5'	10	20	30	40	50
ATCTCTATCA	TTAGAGATCT	GAATATGAAA	TACTTGTCAA	AGTGAATGAA	
	60	70	80	90	100
AATTTNNTAA	ATTATGTATG	GTAAACATCT	TTAAATTGCT	TATTTTAA	
	110	120	130	140	150
TTGCCATGTT	TGTGTCCCAG	TTTGCATTAA	CAAATAGTTT	GAGAACTATG	
	160	170	180	190	200
35	TTGGAAAAAA	AAATAACAAT	TTTATTCTTC	TTTCTCCAGG	CTAGAAGAAC

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1	210	220	230	240	250
	AAAAGAATAT	CTTGTCAGAA	TTTCAAAGAG	ATTTAAATGA	ATTTGTTTTA
	260	270	280	290	300
	TGGTTGGAGG	AAGCAGATAA	CATTGCTAGT	ATCCCACTTG	AACCTGGAAA
	310	320	330	340	350
5	AGAGCAGCAA	CTAAAAGAAA	AGCTTGAGCA	AGTCAAGGTA	ATTTTATTTT
	360	370	380	390	400
	CTCAAATCCC	CCAGGGCCTG	CTTGCAATAA	GAAGTATATG	AATCTATTTT
	410	420	430	440	450
	TTAATTCAAT	CATTGGTTTT	CTGCCCATT	GGTTATTCAT	AGTTCCTTGC
	460	470	480	490	500
	TAAAGTGTTT	TTCTCACAAC	TTTATTTCTT	CTTAACCCTG	CAGTTCTGAA
	510	520	530	540	550
10	CCAGTGCACA	TAAGAACATA	TGTATATATG	TGTGTGTGTG	TATTTATATA
	560	570	580	590	600
	TACACACACA	CATATTGCAT	CTATACATCT	ACACATATAG	ATGTATAGAT
	610	620	630	640	650
	TCAATATGTC	TAAAAATGTA	TATAATTCAC	AGTTTTTATC	TTTGATTGTA
	660	670	680		
	ATATTTAAGG	GACTGAGACT	CACACTCATA	TACTTTT-3'	

15 and fragments and derivatives thereof, said fragments and derivatives complementary to the sense and anti-sense strands of the gene coding for dystrophin, said fragments and derivatives capable of annealing to said strands of the dystrophin gene and amplifying dystrophin sequences.

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